Search Notes

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 14:23:24 ; Search time 42 Seconds
(without alignments)
207.951 Million cell updates/sec

Title: US-10-659-782B-32
Perfect score: 620
Sequence: 1 MPSPGTVCSLLLLGMLWLDL.....PPSSRERSRRSHQPSCSPEL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	198	31.9	117	3	US-09-046-479-2	Sequence 2, Appli
2	198	31.9	117	3	US-08-822-897C-2	Sequence 2, Appli
3	198	31.9	117	4	US-09-608-810A-4	Sequence 4, Appli
4	198	31.9	117	4	US-09-404-417A-2	Sequence 2, Appli
5	198	31.9	117	4	US-09-794-987-2	Sequence 2, Appli
6	74	11.9	597	4	US-09-949-016-7800	Sequence 7800, Ap
7	73.5	11.9	569	4	US-09-252-991A-27248	Sequence 27248, A
8	71.5	11.5	201	4	US-09-902-540-13645	Sequence 13645, A
9	71.5	11.5	643	4	US-09-252-991A-21569	Sequence 21569, A
10	70.5	11.4	382	4	US-09-949-016-10513	Sequence 10513, A
11	70.5	11.4	383	2	US-08-391-916A-4	Sequence 4, Appli
12	70.5	11.4	383	4	US-09-764-803B-23	Sequence 23, Appl
13	70.5	11.4	393	4	US-09-248-796A-19806	Sequence 19806, A
14	70	11.3	18	4	US-09-404-417A-11	Sequence 11, Appl
15	69.5	11.2	835	4	US-09-949-016-7379	Sequence 7379, Ap
16	68	11.0	995	5	PCT-US95-04910-14	Sequence 14, Appl
17	67.5	10.9	168	4	US-09-252-991A-17387	Sequence 17387, A
18	67	10.8	396	4	US-09-134-000C-4470	Sequence 4470, Ap
19	67	10.8	449	2	US-08-489-666C-3	Sequence 3, Appli
20	67	10.8	449	2	US-08-911-092-3	Sequence 3, Appli
21	67	10.8	449	2	US-08-485-001B-3	Sequence 3, Appli
22	67	10.8	449	3	US-08-454-121A-3	Sequence 3, Appli
23	67	10.8	449	3	US-08-482-161B-3	Sequence 3, Appli
24	67	10.8	449	3	US-09-057-963A-2	Sequence 2, Appli
25	67	10.8	973	4	US-09-252-991A-23944	Sequence 23944, A
26	66.5	10.7	263	2	US-08-391-916A-8	Sequence 8, Appli
27	66.5	10.7	311	2	US-08-391-916A-6	Sequence 6, Appli
28	66	10.6	508	4	US-09-252-991A-27892	Sequence 27892, A
29	66	10.6	1122	4	US-09-042-460-2	Sequence 2, Appli
30	65	10.5	303	6	5340934-13	Patent No. 5340934
31	65	10.5	303	6	5340934-13	Patent No. 5340934
32	65	10.5	431	3	US-08-845-258-34	Sequence 34, Appl
33	65	10.5	431	3	US-08-990-571-34	Sequence 34, Appl
34	65	10.5	431	3	US-08-723-142A-34	Sequence 34, Appl
35	65	10.5	431	4	US-09-528-784A-34	Sequence 34, Appl
36	65	10.5	431	4	US-09-569-098A-34	Sequence 34, Appl
37	65	10.5	449	1	US-07-917-722-2	Sequence 2, Appli
38	65	10.5	466	3	US-09-724-864-44	Sequence 44, Appl
39	64.5	10.4	263	4	US-09-252-991A-20756	Sequence 20756, A
40	64	10.3	312	4	US-09-902-540-14391	Sequence 14391, A
41	64	10.3	637	4	US-09-949-016-10956	Sequence 10956, A
42	64	10.3	1062	4	US-09-902-540-16313	Sequence 16313, A
43	63.5	10.2	250	4	US-09-248-796A-19737	Sequence 19737, A
44	63.5	10.2	334	3	US-09-218-363-11	Sequence 11, Appl
45	63	10.2	193	4	US-09-252-991A-24544	Sequence 24544, A

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 2
US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
;  GENERAL INFORMATION:
;    APPLICANT:  Sheppard, Paul O.
;    APPLICANT:  Deisher, Theresa A.
;    TITLE OF INVENTION:  MOTILIN HOMOLOGS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,897C
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  97-04
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-822-897C-2

  Query Match             31.9%;  Score 198;  DB 3;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 3e-17;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 3
US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
;  APPLICANT:  Sheppard, Paul O.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Deisher, Theresa A.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION:  SGIP PEPTIDES
;  FILE REFERENCE:  99-51
;  CURRENT APPLICATION NUMBER: US/09/608,810A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER:  60/141,592
;  PRIOR FILING DATE:  1999-06-30
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(23)
US-09-608-810A-4

  Query Match             31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 3e-17;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 4
US-09-404-417A-2
; Sequence 2, Application US/09404417A
; Patent No. 6627729
; GENERAL INFORMATION:
;  APPLICANT:  Sheppard, Paul O.
;  APPLICANT:  Deisher, Theresa A.
;  APPLICANT:  Jaspers, Stephen R.
;  TITLE OF INVENTION:  TML PEPTIDES
;  FILE REFERENCE:  97-04C1
;  CURRENT APPLICATION NUMBER: US/09/404,417A
;  CURRENT FILING DATE:  1999-09-23
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-404-417A-2

  Query Match             31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 3e-17;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 5
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. 6838438
;   GENERAL INFORMATION:
;        APPLICANT: Sheppard, Paul O.
;                   Deisher, Theresa A.
;        TITLE OF INVENTION: MOTILIN HOMOLOGS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
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;              APPLICATION NUMBER: US/09/794,987
;              FILING DATE: 27-Feb-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/046,479
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Sawislak, Deborah A
;              REGISTRATION NUMBER: 37,438
;              REFERENCE/DOCKET NUMBER: 97-04
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 206-442-6672
;              TELEFAX: 206-442-6678
;              TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 117 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         FRAGMENT TYPE: internal
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

  Query Match             31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 3e-17;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 6
US-09-949-016-7800
; Sequence 7800, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7800
;   LENGTH: 597
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7800

  Query Match             11.9%;  Score 74;  DB 4;  Length 597;
  Best Local Similarity   27.4%;  Pred. No. 1.7;
  Matches   34;  Conservative   15;  Mismatches   35;  Indels   40;  Gaps    6;

Qy          3 SPGTVCS-------------LLLLGMLWLDLAMAGS---SFLSPEHQRVQVRP-PHKAP 44
              ||||  |              |:|||:  | | : ||   : |  :: ||:  | |   |
Db        152 SPGTPGSQGPQAAPGESIWMALVLLGLFLLLLLLGSIILALLQRKNYRVRGEPVPEPRP 211

Qy         45 H-------VVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLF 97
                     :  ||   :||             |||  :: |  :  :|:  |  |  : |
Db        212 DSGRDWSVELQELP---ELC------------FSQVIREGGHAVVWAGQLQGKLVAIKAF 256

Qy         98 PPSS 101
              || |
Db        257 PPRS 260


RESULT 7
US-09-252-991A-27248
; Sequence 27248, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 27248
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27248

  Query Match             11.9%;  Score 73.5;  DB 4;  Length 569;
  Best Local Similarity   31.3%;  Pred. No. 1.9;
  Matches   31;  Conservative    9;  Mismatches   34;  Indels   25;  Gaps    4;

Qy          9 SLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQRHLWAS 68
              ||| | | |   : ||| |   |  |:              |||      :|:  ||  |
Db        434 SLLPLAMRWAGRSRAGSEF---ELGRM-------------LPLQ---AAIEESLHLAIS 473

Qy         69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRR 107
                | :   |:   |          ::| ||   :|||| ||
Db        474 AFLREDLDAALRLVAR-----KKLLQRLEADASRERFRR 507


RESULT 8
US-09-902-540-13645
; Sequence 13645, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13645
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-13645

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  Best Local Similarity   27.6%;  Pred. No. 0.76;
  Matches   32;  Conservative   13;  Mismatches   42;  Indels   29;  Gaps    6;

Qy         10 LLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQRHL---- 65
                :||:|:| |  : ||:       |  :  | |::|   ||      |  :  | |
Db          7 VLLVGVLGL-ASSAGA-------QEARRPPEHRSP--TPAWAPRGVLLGVSAQDGLVASQ 56

Qy         66 ----WASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFP------PSSRERSRRSHQP 111
                 |-  | |  ||: : |     :|||      ||      | :  ||   | |
Db         57 TKVQWQFTFYQDRKDAFALLLEGSLSWGL-----AFPDAEEGKPQNAVRSFYQHSP 107
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RESULT 9
US-09-252-991A-21569
; Sequence 21569, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 21569
;   LENGTH: 643
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21569

  Query Match             11.5%;  Score 71.5;  DB 4;  Length 643;
  Best Local Similarity   25.7%;  Pred. No. 4;
  Matches   37;  Conservative   17;  Mismatches   47;  Indels   43;  Gaps    8;

Qy          2 PSPGTV--CSLLLLGML------------WLDLAMAGSSFLSPEHQRVQVRPPHKAPHV 46
              || | :  || :: |               |  |    |:| : | : |: | |   |
Db        389 PSAGQMWSCSQVISGRSSARPRNRLIAEWPWA-LTRPGASSM-PGNSRISVAPWRMA--- 443

Qy         47 VPALPLSNQLCDLEQQRHLW----ASVFSQSTKDSGSDLTVS----GRTWGLRVLNRLFP 98
                          |      | :|      | :|:||  :||  |:       |: ||| |
Db        444 ----------CSRGATRAIWPSRMPSAWSRSTTPAGSTGTIQVGSRRRSKGLRTLGMAAH 493

Qy         99 PSSRERSRRSHQPSC-----SPEL 117
              |  |  ||:  : |      :|:|
Db        494 PGRRAGSRKYTRASAAGARYNPQL 517


RESULT 10
US-09-949-016-10513
; Sequence 10513, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10513
;   LENGTH: 382
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10513

  Query Match             11.4%;  Score 70.5;  DB 4;  Length 382;
  Best Local Similarity   22.0%;  Pred. No. 2.6;
  Matches   27;  Conservative   20;  Mismatches   37;  Indels   39;  Gaps    4;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSN------ 54
              :|     | : :  :   |  :||:  ||   | ||          ||:| |:
Db         61 IPKGAQACQICITYICEEDSYLAGTLGLSAAPQAVQDN---------PAMPTSSGSEGNV 111

Qy         55 QLCDLEQQRHLW----ASVFSQSTKDS-------------------GSDLTVSGRTWGL 90
              :|| ||: : :|    | ::    | |                   |::: ::| |  |
Db        112 KLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLL 171

Qy         91 RVL 93
              : |
Db        172 QNL 174


RESULT 11
US-08-391-916A-4
; Sequence 4, Application US/08391916A
; Patent No. 5856169
;  GENERAL INFORMATION:
;    APPLICANT:  Litwack, Gerald
;    APPLICANT:  Alnemri, Emad S.
;    APPLICANT:  Fernandez-Alnemri, Teresa
;    TITLE OF INVENTION:  ISOFORMS OF HUMAN INTERLEUKIN-1BETA CONVERTING
;    TITLE OF INVENTION:  ENZYME AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5856169ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/391,916A
;      FILING DATE:  21-FEB-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-1464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  383 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-391-916A-4

  Query Match             11.4%;  Score 70.5;  DB 2;  Length 383;
  Best Local Similarity   22.0%;  Pred. No. 2.6;
  Matches   27;  Conservative   20;  Mismatches   37;  Indels   39;  Gaps    4;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSN------ 54
              :|     | : :  :   |  :||:  ||   | ||          ||:| |:
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              :|| ||: : :|    | ::    | |                   |::: ::| |  |
Db        113 KLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLL 172

Qy         91 RVL 93
              : |
Db        173 QNL 175


RESULT 12
US-09-764-803B-23
; Sequence 23, Application US/09764803B
; Patent No. 6759227
; GENERAL INFORMATION:
;  APPLICANT: Van de Craen, Marc
```

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;  APPLICANT:  Declercq, Wim
;  APPLICANT:  Vandenabeele, Peter
;  APPLICANT:  Fiers, Walter
;  TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
;  FILE REFERENCE: 2676-4661US
;  CURRENT APPLICATION NUMBER: US/09/764,803B
;  CURRENT FILING DATE:  2001-01-17
;  PRIOR APPLICATION NUMBER: PCT/EP99/04939
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: EP 98202422.6
;  PRIOR FILING DATE: 1999-07-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(383)
;   OTHER INFORMATION: human capase-1 (genbank)
US-09-764-803B-23

  Query Match             11.4%;  Score 70.5;  DB 4;  Length 383;
  Best Local Similarity   22.0%;  Pred. No. 2.6;
  Matches   27;  Conservative   20;  Mismatches   37;  Indels   39;  Gaps    4;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSN------ 54
              :|      | : :  :   |  :||:  ||   | ||           ||:| |:
Db         62 IPKGAQACQICITYICEEDSYLAGTLGLSAAPQAVQDN---------PAMPTSSGSEGNV 112

Qy         55 QLCDLEQQRHLW----ASVFSQSTKDS--------------------GSDLTVSGRTWGL 90
              :|| ||: : :|    | ::     | |                  |::: ::| |  |
Db        113 KLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLL 172

Qy         91 RVL 93
              : |
Db        173 QNL 175


RESULT 13
US-09-248-796A-19806
; Sequence 19806, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19806
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-19806

  Query Match             11.4%;  Score 70.5;  DB 4;  Length 393;
  Best Local Similarity   31.6%;  Pred. No. 2.7;
  Matches   24;  Conservative   12;  Mismatches   23;  Indels   17;  Gaps    4;

Qy         39 PPHKAPHVVPALP-LSNQLCDLEQQRHLWASVFSQS----------TKDSGSDLTVSGRT 87
              ||  ||  :|:||  |    : :|| ::|::  |||          | || :  | :  |
Db        185 PPPPAPQRLPSLPTYSMPETESQQQHYVWSTQDSQSHHHQVPPSAITTDSSTASTTTRNT 244

Qy         88 WGLRV-----LNRLFP 98
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Db        245 MPFQVSTNIDINR-FP 259


RESULT 14
US-09-404-417A-11
; Sequence 11, Application US/09404417A
; Patent No. 6627729
; GENERAL INFORMATION:
;  APPLICANT:  Sheppard, Paul O.
;  APPLICANT:  Deisher, Theresa A.
;  APPLICANT:  Jaspers, Stephen R.
;  TITLE OF INVENTION:  TML PEPTIDES
;  FILE REFERENCE:  97-04C1
;  CURRENT APPLICATION NUMBER: US/09/404,417A
;  CURRENT FILING DATE:  1999-09-23
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-404-417A-11

  Query Match             11.3%;  Score 70;  DB 4;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 0.038;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         24 GSSFLSPEHQRVQVR 38
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RESULT 15
US-09-949-016-7379
; Sequence 7379, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7379
;   LENGTH: 835
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7379

  Query Match             11.2%;  Score 69.5;  DB 4;  Length 835;
  Best Local Similarity   25.9%;  Pred. No. 10;
  Matches   38;  Conservative   14;  Mismatches   44;  Indels   51;  Gaps    8;

Qy          9 SLLLLG--------------MLWLDLAMAGSSF-------LSPEH-QRVQVR------- 38
              |::|||                |:|| |  | ||         :|:  | :  :
Db         71 SIILLGATGDLAKKYLWQGLFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALESLSC 130

Qy         39 -----PPHKAPHVVPALPLSNQLCDLEQQRHL-WASVFSQSTKDSGSDLTVSGRTWGLRV 92
                  | | | |          :|   | | | |  |  :        ||  : |  :    |||
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Qy         93 LNRLF----PPSSRERSRRSHQPSCSP 115
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Db        180 AGRIFYFSVPPFAYEDIARNINSSCRP 206
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Search completed: July 26, 2005, 14:39:05
Job time : 43 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 14:29:30 ; Search time 155 Seconds
(without alignments)
293.626 Million cell updates/sec

Title: US-10-659-782B-32
Perfect score: 620
Sequence: 1 MPSPGTVCSLLLLGMLWLDL.....PPSSRERSRRSHQPSCSPEL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605.5	97.7	116	17	US-10-659-782A-32	Sequence 32, Appl
2	198	31.9	60	15	US-10-294-191A-3	Sequence 3, Appli
3	198	31.9	91	16	US-10-477-506-2	Sequence 2, Appli
4	198	31.9	117	9	US-09-794-987-2	Sequence 2, Appli
5	198	31.9	117	9	US-09-853-253-2	Sequence 2, Appli
6	198	31.9	117	9	US-09-989-722-268	Sequence 268, App
7	198	31.9	117	9	US-09-989-723-268	Sequence 268, App
8	198	31.9	117	9	US-09-989-279-268	Sequence 268, App
9	198	31.9	117	9	US-09-989-727-268	Sequence 268, App
10	198	31.9	117	9	US-09-989-731-268	Sequence 268, App
11	198	31.9	117	9	US-09-989-732-268	Sequence 268, App
12	198	31.9	117	9	US-09-991-073-268	Sequence 268, App
13	198	31.9	117	9	US-09-990-442-268	Sequence 268, App
14	198	31.9	117	9	US-09-991-163-268	Sequence 268, App
15	198	31.9	117	9	US-09-993-604-268	Sequence 268, App
16	198	31.9	117	9	US-09-990-456-268	Sequence 268, App
17	198	31.9	117	9	US-09-989-721-268	Sequence 268, App
18	198	31.9	117	9	US-09-992-598-268	Sequence 268, App
19	198	31.9	117	9	US-09-989-293A-268	Sequence 268, App
20	198	31.9	117	9	US-09-989-735-268	Sequence 268, App
21	198	31.9	117	9	US-09-990-444-268	Sequence 268, App
22	198	31.9	117	9	US-09-991-181-268	Sequence 268, App
23	198	31.9	117	9	US-09-989-730-268	Sequence 268, App
24	198	31.9	117	9	US-09-990-436-268	Sequence 268, App
25	198	31.9	117	9	US-09-993-687-268	Sequence 268, App
26	198	31.9	117	10	US-09-989-734-268	Sequence 268, App
27	198	31.9	117	10	US-09-997-653-268	Sequence 268, App
28	198	31.9	117	10	US-09-989-724-268	Sequence 268, App
29	198	31.9	117	10	US-09-989-728-268	Sequence 268, App
30	198	31.9	117	10	US-09-990-441-268	Sequence 268, App
31	198	31.9	117	10	US-09-993-667-268	Sequence 268, App
32	198	31.9	117	10	US-09-997-428-268	Sequence 268, App
33	198	31.9	117	10	US-09-997-666-268	Sequence 268, App
34	198	31.9	117	10	US-09-990-438-268	Sequence 268, App
35	198	31.9	117	10	US-09-990-562-268	Sequence 268, App
36	198	31.9	117	10	US-09-990-711-268	Sequence 268, App
37	198	31.9	117	10	US-09-989-726-268	Sequence 268, App
38	198	31.9	117	10	US-09-998-156-268	Sequence 268, App
39	198	31.9	117	10	US-09-990-437-268	Sequence 268, App
40	198	31.9	117	10	US-09-991-157-268	Sequence 268, App
41	198	31.9	117	10	US-09-997-514-268	Sequence 268, App
42	198	31.9	117	10	US-09-997-573-268	Sequence 268, App
43	198	31.9	117	10	US-09-991-172-268	Sequence 268, App
44	198	31.9	117	10	US-09-990-726-268	Sequence 268, App
45	198	31.9	117	10	US-09-997-559-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-10-659-782A-32
; Sequence 32, Application US/10659782A
; Publication No. US20050059015A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,
; TITLE OF INVENTION: Monitoring and Treating Obesity and/or Diabetes
; FILE REFERENCE: 28238
; CURRENT APPLICATION NUMBER: US/10/659,782A
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-782A-32

Query Match 97.7%; Score 605.5; DB 17; Length 116;
Best Local Similarity 99.1%; Pred. No. 9.9e-58;
Matches 116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60

Qy         61 QQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 117
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Db         61 QQRH-WASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 116
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RESULT 2
US-10-294-191A-3

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; Sequence 3, Application US/10294191A
; Publication No. US20030211512A1
; GENERAL INFORMATION:
;  APPLICANT: Rothschild, Max F.
;  APPLICANT:  Kim, Kwan Suk
;  APPLICANT:  Anderson, Lloyd L.
;  TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
;  FILE REFERENCE: P05408US1
;  CURRENT APPLICATION NUMBER: US/10/294,191A
;  CURRENT FILING DATE:  2002-11-14
;  PRIOR APPLICATION NUMBER: US 60/333,222
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 60
;   TYPE: PRT
;   ORGANISM: Human
US-10-294-191A-3

  Query Match             31.9%;  Score 198;  DB 15;  Length 60;
  Best Local Similarity   88.6%;  Pred. No. 8.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |    | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 3
US-10-477-506-2
; Sequence 2, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
;  APPLICANT: Chopin, Lisa K
;  APPLICANT:  Jeffery, Penelope L
;  APPLICANT:  Herington, Adrian C
;  TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
;  FILE REFERENCE: 225181
;  CURRENT APPLICATION NUMBER: US/10/477,506
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: PR9567
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: PR4919
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: PCT/AU02/000582
;  PRIOR FILING DATE: 2002-05-10
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 91
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-477-506-2

  Query Match             31.9%;  Score 198;  DB 16;  Length 91;
  Best Local Similarity   88.6%;  Pred. No. 1.4e-13;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 4
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
;   GENERAL INFORMATION:
;        APPLICANT: Sheppard, Paul O.
;                   Deisher, Theresa A.
;        TITLE OF INVENTION: MOTILIN HOMOLOGS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/794,987
;             FILING DATE: 27-Feb-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/046,479
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sawislak, Deborah A
;             REGISTRATION NUMBER: 37,438
;             REFERENCE/DOCKET NUMBER: 97-04
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-442-6672
;             TELEFAX: 206-442-6678
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 117 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

  Query Match             31.9%;  Score 198;  DB 9;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 1.9e-13;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 5
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
;  APPLICANT: JASPERS, STEPHEN
;  APPLICANT:  SHEPPARD, PAUL
;  APPLICANT:  DEISHER, THERESA
;  APPLICANT:  BISHOP, PAUL
;  TITLE OF INVENTION: Zsig33-like Peptides
;  FILE REFERENCE: 00-30
;  CURRENT APPLICATION NUMBER: US/09/853,253
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: 60/203,300
;  PRIOR FILING DATE: 2000-05-11
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-853-253-2

  Query Match             31.9%;  Score 198;  DB 9;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 1.9e-13;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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RESULT 6
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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;  APPLICANT: Ashkenazi,Avi J.
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;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
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;  APPLICANT:  Roy, Margaret Ann
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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C62
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 9
US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 31.9%; Score 198; DB 9; Length 117;
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Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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; Sequence 268, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 11
US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
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RESULT 12
US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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Query Match 31.9%; Score 198; DB 9; Length 117;
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; APPLICANT: Ashkenazi,Avi J.
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 14
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT APPLICATION NUMBER: US/09/991,163
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Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 15
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
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; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 9; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.9e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Job time : 157 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 14:11:02 ; Search time 174 Seconds
(without alignments)
260.063 Million cell updates/sec

Title: US-10-659-782B-32
Perfect score: 620
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	198	31.9	91	6	AAE33410	Aae33410 Human exo
3	198	31.9	117	2	AAW87991	Aaw87991 Protein d
4	198	31.9	117	3	AAY87236	Aay87236 Human sig
5	198	31.9	117	4	AAB20101	Aab20101 Zsig33 pr
6	198	31.9	117	4	AAB62649	Aab62649 Human zsi
7	198	31.9	117	4	AAM38890	Aam38890 Human pol
8	198	31.9	117	4	AAB60511	Aab60511 Human ghr
9	198	31.9	117	5	ABB78319	Abb78319 Amino aci
10	198	31.9	117	5	AAE23838	Aae23838 Human zsi
11	198	31.9	117	5	AAE15883	Aae15883 Human zsi
12	198	31.9	117	6	ABU58046	Abu58046 Human PRO
13	198	31.9	117	6	ABU59124	Abu59124 Novel hum
14	198	31.9	117	6	ABU82636	Abu82636 Human sec
15	198	31.9	117	6	ABO17836	Abo17836 Novel hum
16	198	31.9	117	6	ABU60555	Abu60555 Human sec
17	198	31.9	117	6	ABU13937	Abu13937 Human PRO
18	198	31.9	117	6	ABU81090	Abu81090 Human PRO
19	198	31.9	117	6	ABU72522	Abu72522 Novel hum
20	198	31.9	117	6	ABU66790	Abu66790 Human PRO
21	198	31.9	117	6	ABU59871	Abu59871 Novel sec
22	198	31.9	117	6	ABU59271	Abu59271 Human sec
23	198	31.9	117	6	ABO25968	Abo25968 Human PRO
24	198	31.9	117	6	ABO25061	Abo25061 Human sec
25	198	31.9	117	6	ABU58977	Abu58977 Human sec
26	198	31.9	117	6	ABU92355	Abu92355 Novel hum
27	198	31.9	117	6	AAE33409	Aae33409 Human pre
28	198	31.9	117	6	ABU59420	Abu59420 Novel hum
29	198	31.9	117	6	ABU67066	Abu67066 Human sec
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38	198	31.9	117	6	ADA61665	Ada61665 Homo sapi
39	198	31.9	117	6	ADB19450	Adb19450 Novel hum
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45	198	31.9	117	6	ADA21465	Ada21465 Human sec

ALIGNMENTS

RESULT 1
ADK66754
ID ADK66754 standard; protein; 60 AA.
XX
AC ADK66754;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human ghrelin protein #1.
XX
KW Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;
KW breeding; human.
XX
OS Homo sapiens.
XX
PN US2003211512-A1.
XX
PD 13-NOV-2003.
XX
PF 14-NOV-2002; 2002US-0029419i.
XX
PR 14-NOV-2001; 2001US-0333222P.
XX
PA (ROTH/) ROTHSCHILD M F.
PA (KIMK/) KIM K.
PA (ANDE/) ANDERSON L L.
XX
PI Rothschild MF, Kim K, Anderson LL;
XX
DR WPI; 2004-010667/01.
XX
PT Screening animals (i.e. pigs) to determine those more likely to produce
PT desired growth, appetite and fatness to optimize breeding and selection
PT techniques comprises detecting the presence of a polymorphism in the
PT Ghrelin gene.
XX
PS Disclosure; SEQ ID NO 3; 24pp; English.
XX
CC The present invention relates to a method of screening animals to
CC determine those more likely to produce desired growth, appetite and
CC fatness which involves obtaining a sample of genetic material from the
CC animal and assaying for the presence of a genotype in the animal which is
CC associated with favourable growth, appetite and fatness, the genotype
CC characterised by a polymorphism in the ghrelin gene. The composition and
CC methods are useful in screening animals (i.e. pigs) to determine those
CC more or less likely to produce desired growth, appetite and fatness to
CC optimise breeding and selection techniques. The present sequence is human
CC ghrelin protein of the invention.

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SQ   Sequence 60 AA;

  Query Match             31.9%;  Score 198;  DB 8;  Length 60;
  Best Local Similarity   88.6%;  Pred. No. 1e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 2
AAE33410
ID   AAE33410 standard; protein; 91 AA.
XX
AC   AAE33410;
XX
DT   02-APR-2003  (first entry)
XX
DE   Human exon 3-deleted ghrelin protein.
XX
KW   Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
KW   breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
KW   cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO200290387-A1.
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PD   14-NOV-2002.
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PF   10-MAY-2002; 2002WO-AU000582.
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PR   10-MAY-2001; 2001AU-00004919.
PR   17-DEC-2001; 2001AU-00009567.
XX
PA   (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI   Chopin LK,  Jeffery PL,  Herington AC;
XX
DR   WPI; 2003-111957/10.
DR   N-PSDB; AAD50726.
XX
PT   Identifying a cancer cell or tissue for treating prostate, ovarian,
PT   breast cancer, or benign prostatic hyperplasia, by detecting the
PT   expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
PT   1b proteins or nucleic acids.
XX
PS   Claim 14; Page 34; 50pp; English.
XX
CC   The invention relates to a method for identifying a cancer cell or tissue
CC   of the reproductive system by detecting expression of a ghrelin, an exon-
CC   3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The
CC   antibodies, exon 3-deleted form of preproghrelin and antagonists are
CC   useful for treating cancer of the reproductive system such as prostate,
CC   ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign
CC   prostatic hyperplasia. The present sequence is human exon 3-deleted
CC   ghrelin protein
XX
SQ   Sequence 91 AA;

  Query Match             31.9%;  Score 198;  DB 6;  Length 91;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 3
AAW87991
ID   AAW87991 standard; protein; 117 AA.
XX
AC   AAW87991;
XX
DT   07-APR-1999  (first entry)
XX
DE   Protein designated zsig33.
XX
KW   Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW   nutrient absorption regulation; obesity; metabolic disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "signal peptide"
FT   Protein         24. .117
FT                   /note= "mature protein"
XX
PN   WO9842840-A1.
XX
PD   01-OCT-1998.
XX
PF   23-MAR-1998;   98WO-US005620.
XX
PR   24-MAR-1997;   97US-0041102P.
PR   24-MAR-1997;   97US-00822897.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Deisher TA;
XX
DR   WPI; 1999-070071/06.
DR   N-PSDB; AAX04550.
XX
PT   Human polypeptide having homology to motilin, zsig33 - useful e.g. to
PT   treat gastrointestinal motility disorders, obesity etc. and to identify
PT   antagonists to treat gastrointestinal hypermotility.
XX
PS   Claim 13; Page 55-56; 69pp; English.
XX
CC   The present sequence represents a protein designated Zsig33. The nucleic
CC   acids are strongly expressed in stomach tissue. The polypeptide (or
CC   allelic variants/orthologs) can be used to stimulate gastric motility,
CC   measured as increased transit time or gastric emptying of an ingested
CC   substance in mammals. The products are used to treat disorders associated
CC   with gastrointestinal cell contractility, secretion of digestive
CC   enzymes/acids, gastrointestinal motility, recruitment of digestive
CC   enzymes, gastrointestinal inflammation, reflux disease and nutrient
CC   absorption regulation. Zsig33 polypeptides may also be important
CC   neurologically, since the family of gut-brain peptides to which the
CC   homologous protein motilin belongs has been associated with neurological
CC   and CNS functions. They may therefore be used e.g. to regulate satiety or
CC   treat obesity and other metabolic disorders where neurological feedback
CC   modulates nutritional absorption. They are useful to identify zsig33
CC   agonists, antagonists and ligands and to produce antibodies
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 2;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 4
AAY87236
ID   AAY87236 standard; protein; 117 AA.
XX
AC   AAY87236;
```

```
XX
DT   11-MAY-2000  (first entry)
XX
DE   Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
XX
KW   Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW   inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW   antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW   antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW   reproductive disorder; developmental disorder; arteriosclerosis;
KW   cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW   asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW   Parkinson's disease; Huntington's diseases; ovulatory defect;
KW   muscular dystrophy.
XX
OS   Homo sapiens.
XX
PN   WO200000610-A2.
XX
PD   06-JAN-2000.
XX
PF   25-JUN-1999;   99WO-US014484.
XX
PR   26-JUN-1998;   98US-0090762P.
PR   31-JUL-1998;   98US-0094983P.
PR   01-OCT-1998;   98US-0102686P.
PR   11-DEC-1998;   98US-0112129P.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Tang YT,  Gorgone GA,  Corley NC,  Guegler KJ,  Baughn MR;
PI   Akerblom IE,  Au-Young J,  Yue H,  Patterson C,  Reddy R,  Hillman JL;
PI   Bandman O;
XX
DR   WPI; 2000-160673/14.
DR   N-PSDB; AAZ98121.
XX
PT   New human signal peptide-containing proteins useful in treatment,
PT   prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT   disease.
XX
PS   Claim 1; Page 168-169; 327pp; English.
XX
CC   AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC   human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC   anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC   neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC   used in gene therapy. HSPPs can be used to treat or prevent disorders
CC   associated with decreased activity or function of HSPP. Antagonists of
CC   HSPP are used to treat or prevent disorders associated with increased
CC   activity or function of HSPP. Such diseases include cell proliferation
CC   (including cancer), inflammation, cardiovascular, neurological,
CC   reproductive or developmental disorders, (e.g. arteriosclerosis,
CC   cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC   asthma, Crohn's disease, microbial or other infections, congestive or
CC   ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC   diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC   nucleic acids can be used for the recombinant production of HSPP, for
CC   detecting HSPP in standard hybridisation and amplification assays (for
CC   diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC   or ribozyme therapeutics, for detecting related sequences or genetic
CC   variations, and for chromosomal mapping. HSPP are also used to raise
CC   specific antibodies (Ab) and to screen for agonists and antagonists
CC   (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
CC   -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC   competitive drug screens, and for purification of HSPP from natural
CC   sources
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 3;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 5
AAB20101
ID   AAB20101 standard; protein; 117 AA.
XX
AC   AAB20101;
XX
DT   23-APR-2001  (first entry)
XX
DE   Zsig33 protein.
XX
KW   SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW   nutritional absorption modulator; growth hormone secretagogue; therapy;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .117
FT                   /label= Mature_protein
FT   Peptide         24. .34
FT                   /label= SGIP_peptide
FT                   /note= "this peptide is claimed in Claim 1"
XX
PN   WO200100830-A1.
XX
PD   04-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018306.
XX
PR   30-JUN-1999;   99US-00345157.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Jaspers SR,  Deisher TA,  Bishop PD;
XX
DR   WPI; 2001-123010/13.
DR   N-PSDB; AAF30033.
XX
PT   Novel variants of SGIP peptides for modulating contractility in duodenum
PT   or jejunum tissue, pancreatic secretion of hormones and digestive
PT   enzymes, inducing growth hormone secretion or modulating gastric
PT   emptying.
XX
PS   Disclosure; 54; 61pp; English.
XX
CC   The present sequence is that of zsig33, a secreted protein with homology
CC   to motilin (see AAB20102). Zsig33 is expressed at high levels in the
CC   stomach, and at lower levels in the small intestine and pancreas. A novel
CC   peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP
CC   is a ligand for growth hormone secretagogue receptor, and is therefore
CC   useful for modulating secretion of growth hormone and insulin like growth
CC   factor 1. SGIP, and variant SGIP peptides, are used in claimed methods
CC   for stimulating contractability in duodenum or jejunum tissue, modulating
CC   pancreatic secretion of hormones and digestive enzymes, inducing growth
CC   hormone secretion, and modulating gastric emptying
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
```

```
RESULT 6
AAB62649
ID   AAB62649 standard; protein; 117 AA.
XX
AC   AAB62649;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Human zsig33 polypeptide.
XX
KW   zsig33; signal transduction; hormone; enzyme; neural development;
KW   gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW   insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW   glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
KW   G-protein coupled receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         24. .37
FT                   /note= "specifically claimed fragment that binds to the
FT                   GHS-R"
XX
PN   WO200138355-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032074.
XX
PR   22-NOV-1999;   99US-0166765P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Jaspers SR,  Deisher TA,  Bishop PD;
XX
DR   WPI; 2001-355879/37.
DR   N-PSDB; AAF83678.
XX
PT   Forming reversible peptide receptor complex for purifying cell and
PT   peptides, stimulating signal transduction and modulating hormone
PT   secretion, involves contacting a receptor with zsig33 polypeptide.
XX
PS   Claim 1; Page 93-94; 111pp; English.
XX
CC   The invention relates to a method of forming a reversible peptide-
CC   receptor complex that involves providing an immobilized receptor, and
CC   contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC   of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC   is useful for purifying cells, purifying a peptide, stimulating signal
CC   transduction in a cell expressing a receptor. It is also useful for
CC   modulating secretion of hormones, neural development and/or utilization,
CC   gastric contractility, nutrient uptake, secretion of digestive and
CC   pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC   -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC   hormone secretion in a mammal having a disease associated with abnormal
CC   levels of growth hormone, such as osteoporosis, bone repair, bone
CC   remodeling, low osteoblast levels, cartilage repair and remodeling,
CC   skeletal dysplasia, immune suppression, obesity, growth retardation,
CC   protein catabolic responses after surgery, cachexia, protein loss,
CC   dwarfism, wound healing and ovulation induction, treating a mammal having
CC   a metabolic disorder requiring neurological feedback, such as satiety
CC   regulation, glucose absorption and metabolism and neuropathy-associated
CC   gastrointestinal disorders, and stimulating glucose-induced insulin
CC   release in a mammal. The present sequence represents the human zsig33
CC   polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 7
AAM38890
ID   AAM38890 standard; protein; 117 AA.
XX
AC   AAM38890;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 2035.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI58046.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 3; SEQ ID NO 2035; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 117 AA;
```

```
  Query Match           31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity  88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 8
AAB60511
ID   AAB60511 standard; protein; 117 AA.
XX
AC   AAB60511;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human ghrelin preproprotein, SEQ ID NO:5.
XX
KW   Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW   calcium concentration elevation; infant growth disorder;
KW   growth hormone deficiency.
XX
OS   Homo sapiens.
XX
PN   WO200107475-A1.
XX
PD   01-FEB-2001.
XX
PF   24-JUL-2000; 2000WO-JP004907.
XX
PR   23-JUL-1999;   99JP-00210002.
PR   29-NOV-1999;   99JP-00338841.
PR   26-APR-2000; 2000JP-00126623.
XX
PA   (KANG/) KANGAWA K.
XX
PI   Kangawa K,  Kojima M,  Hosoda H,  Matsuo H,  Minamitake Y;
XX
DR   WPI; 2001-159704/16.
DR   N-PSDB; AAF59645.
XX
PT   New peptide compounds which induce growth hormone secretion and elevate
PT   cell calcium concentrations, useful in treatment and diagnosis of infant
PT   growth disorders.
XX
PS   Claim 3; Page 182; 210pp; Japanese.
XX
CC   The invention relates to a novel peptide compound or its salt which
CC   induces the secretion of growth hormone and/or elevates calcium ion
CC   concentration in cells. The peptides are ghrelin homologues and are
CC   characterised in that at least one amino acid has been substituted by a
CC   modified amino acid and/or a non-amino acid compound. The invention also
CC   encompasses the unmodified peptides; the DNA encoding the peptides;
CC   vectors and host cells comprising such DNA; a method of producing the
CC   peptides comprising recombinant production, optionally followed by
CC   chemical modification; an antibody specific for a peptide of the
CC   invention; and an assay and kit for detecting the peptides. The peptides
CC   of the invention are useful for treating and/or diagnosing diseases
CC   caused by a deficiency in growth hormone expression or activity. In
CC   particular, they are useful for promoting infant growth due to growth
CC   hormone deficiency. The compounds of the invention are safe with no
CC   accompanying side effects. The present sequence represents a ghrelin-type
CC   growth hormone secretagogue (GHS) precursor protein of the invention
XX
SQ   Sequence 117 AA;

  Query Match           31.9%;  Score 198;  DB 4;  Length 117;
  Best Local Similarity  88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 9
ABB78319
ID   ABB78319 standard; protein; 117 AA.
XX
AC   ABB78319;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Amino acid sequence of a human zsig33.
XX
KW   Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "signal peptide"
FT   Protein         24. .119
FT                   /note= "mature protein"
XX
PN   US6420521-B1.
XX
PD   16-JUL-2002.
XX
PF   30-JUN-2000; 2000US-00608810.
XX
PR   30-JUN-1999;   99US-0141592P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Jaspers SR,  Deisher TA,  Bishop PD;
XX
DR   WPI; 2002-634794/68.
DR   N-PSDB; ABV72214.
XX
PT   New Short Gastrointestinal Peptide, which has homology to motilin, useful
PT   for preventing, diagnosing and treating gastrointestinal disorders.
XX
PS   Disclosure; Col 39-40; 23pp; English.
XX
CC   The present sequence represents human zsig33. The specification describes
CC   a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC   SGIP has homology to motilin. The SGIP peptide may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate SGIP expression. For example, SGIP may be used to treat
CC   disorders associated with decreased expression by rectifying mutations or
CC   deletions in a patient's genome that affect the activity of SGIP by
CC   expressing inactive proteins or to supplement the patients own production
CC   of SGIP. SGIP may also be used as an antigen in the production of
CC   antibodies against SGIP and in assays to identify modulators of SGIP
CC   expression and activity. The anti-SGIP antibodies, agonists and
CC   antagonists may also be used to regulate expression and activity. The
CC   anti-SGIP antibodies may also be used as diagnostic agents for detecting
CC   the presence of SGIP in samples
XX
SQ   Sequence 117 AA;

  Query Match           31.9%;  Score 198;  DB 5;  Length 117;
  Best Local Similarity  88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 10
AAE23838
ID   AAE23838 standard; protein; 117 AA.
XX
```

```
AC   AAE23838;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human zsig33 protein.
XX
KW   Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW   growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW   protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS   Homo sapiens.
XX
PN   US2002055156-A1.
XX
PD   09-MAY-2002.
XX
PF   10-MAY-2001; 2001US-00853253.
XX
PR   11-MAY-2000; 2000US-0203300P.
XX
PA   (JASP/) JASPERS S R.
PA   (SHEP/) SHEPPARD P O.
PA   (DEIS/) DEISHER T A.
PA   (BISH/) BISHOP P D.
XX
PI   Jaspers SR,  Sheppard PO,  Deisher TA,  Bishop PD;
XX
DR   WPI; 2002-443750/47.
DR   N-PSDB; AAD38238.
XX
PT   ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT   contractility, nutrient uptake, growth hormones and/or secretion of
PT   digestive/pancreatic enzymes and hormones.
XX
PS   Disclosure; Page 27; 34pp; English.
XX
CC   The invention relates to zsig33-like peptides and their corresponding
CC   nucleic acids and methods for modulating gastric contractility, nutrient
CC   uptake, growth hormones, secretion of digestive enzymes and hormones. The
CC   sequences of the invention are used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate ZSIG33 expression.
CC   The nucleic acids of the invention and their complements are used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acids in samples, and therefore which patients may be in
CC   need of restorative therapy. The ZSIG33 peptides are used as antigens in
CC   the production of antibodies against ZSIG33 and in assays to identify
CC   modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC   and antagonists are used to down regulate expression and activity. The
CC   anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC   the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC   assay (ELISA)). The peptides and nucleic acids of the invention are used
CC   to modulate gastric contractility, nutrient uptake, growth hormones, the
CC   secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC   and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC   and zsig33-like peptide is used in protein therapy. The present sequence
CC   is human zsig33 protein
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 5;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | ||
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 11
AAE15883
ID   AAE15883 standard; protein; 117 AA.
XX
AC   AAE15883;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human zsig33 protein.
XX
KW   Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW   infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW   adsorption enhancer; gastrointestinal disease; growth related disease;
KW   inflammation; gene therapy; growth regulation; blood vessel formation;
KW   HIV; zsig33 protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .117
FT                   /note= "Human mature zsig33 protein"
XX
PN   WO200187933-A2.
XX
PD   22-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US015091.
XX
PR   11-MAY-2000; 2000US-00569271.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Jaspers SR,  Sheppard PO,  Deisher TA,  Bishop PD;
XX
DR   WPI; 2002-082982/11.
DR   N-PSDB; AAD25759.
XX
PT   New polypeptides, useful for modulating gastric contractility, nutrient
PT   uptake, pancreatic secretion of hormones, digestive enzymes and treating
PT   gastrointestinal and growth related diseases, comprises zsig33-like
PT   peptides.
XX
PS   Disclosure; Page 80-81; 89pp; English.
XX
CC   The invention relates to zsig33-like peptides (ZS33LP) including zsig33-
CC   linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon
CC   peptides and nucleic acid molecules encoding such zsig33-like peptides.
CC   ZS33LP peptides activate the immune system in boosting immunity to
CC   infectious diseases, treating immunocompromised patients such as human
CC   immunodeficiency virus (HIV) patients, in improving vaccines and in
CC   treatment of bacterial, viral, protozoal and fungal infections. Peptides
CC   of the invention are used to identify and isolate receptors involved in
CC   growth regulation in the liver, blood vessel formation and other
CC   developmental processes. They are useful for evaluating functions of
CC   hypothalamus-pituitary-adrenal axis, to modulate growth and/or
CC   differentiation of tumour cells, as additives to anti- hypoglycaemic
CC   preparations containing glucose and as adsorption enhancers for oral
CC   drugs which require fast nutrient action and to stimulate glucose-induced
CC   insulin release. They are also useful as research reagents for the
CC   expansion, differentiation, growth factor and hormone secretion and/or
CC   cell-cell interactions of tissues associated with gastrointestinal
CC   system, brain and central nervous system. These molecules are useful for
CC   treating dysfunction associated with contractile tissues or to suppress
CC   or enhance contractility in vivo and to treat gastrointestinal and growth
CC   related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
CC   useful for treating disorders associated with gastrointestinal
CC   contractility, secretion of digestive enzymes, hormone and acids,
CC   secretion of hormones in the pancreas and/or brain, gastrointestinal
CC   motility, recruitment of digestive enzymes, inflammation and regulation
CC   of nutrient absorption. Sequences of the invention are useful in gene
CC   therapy. The present sequence is human zsig33 protein
XX
SQ   Sequence 117 AA;

  Query Match             31.9%;  Score 198;  DB 5;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44


RESULT 12
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ID   ABU58046 standard; protein; 117 AA.
XX
AC   ABU58046;
XX
DT   14-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #78.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027163-A1.
XX
PD   06-FEB-2003.
XX
PF   15-NOV-2001; 2001US-00997666.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
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PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
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PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
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  Best Local Similarity   88.6%;  Pred. No. 2.4e-14;
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Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
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ID   ABU59124 standard; protein; 117 AA.
XX
AC   ABU59124;
XX
DT   28-APR-2003  (first entry)
XX
DE   Novel human secreted or transmembrane protein PRO1066.
XX
KW   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW   cardiac insufficiency disorder; cancer; tumour; immune response;
KW   adrenal cortical capillary endothelial growth; c-fos induction;
KW   vascular endothelial growth factor inhibition; VEGF inhibition;
KW   endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW   retinal neurons cell survival; rod photoreceptor cell survival;
KW   retinal disorder; retinitis pigmentosum; kidney disorder;
KW   mammalian kidney mesangial cell proliferation; Berger disease;
KW   dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW   chondrocyte redifferentiation; sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002132252-A1.
XX
PD   19-SEP-2002.
XX
PF   14-NOV-2001; 2001US-00990442.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
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PR 17-JUN-1998; 98US-0089599P.
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PR 16-SEP-1998; 98WO-US019330.
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PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
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PR 02-JUN-1999; 99WO-US012252.
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PR 06-JAN-2000; 2000WO-US000219.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-247083/24.
DR N-PSDB; ABX80294.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 12; Fig 186; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 117 AA;

Query Match 31.9%; Score 198; DB 6; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.4e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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Db 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44

RESULT 14
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XX
AC ABU82636;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1066.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003032023-A1.
XX
PD 13-FEB-2003.
XX
PF 14-NOV-2001; 2001US-00990711.
XX
PR 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
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PR 02-JUN-1998; 98US-0087609P.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
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PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
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PR 22-FEB-2000; 2000WO-US004414.
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PR 24-FEB-2000; 2000WO-US005004.
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Query Match 31.9%; Score 198; DB 6; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.4e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 15
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XX
DT 26-AUG-2003 (first entry)
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XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
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PD 13-FEB-2003.
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PF 06-MAY-2002; 2002US-00140474.
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XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24073.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 442; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 117 AA;

Query Match 31.9%; Score 198; DB 6; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.4e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Job time : 177 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 14:19:28 ; Search time 40 Seconds
(without alignments)
281.434 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	158	25.5	117	1	B59316	ghrelin precursor
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5	73	11.8	573	2	JC4335	anti-mullerian hor
6	73	11.8	725	1	E64211	virulence-associat
7	72.5	11.7	555	2	H83043	hypothetical prote
8	72	11.6	666	2	T22943	hypothetical prote
9	71.5	11.5	764	2	I48882	thyrotropin recept
10	70.5	11.4	309	2	S77905	lyase - Pseudomona
11	70.5	11.4	383	2	A56084	interleukin-1beta
12	69	11.1	302	2	H96792	unknown protein F1
13	69	11.1	1487	2	S62048	probable membrane
14	68	11.0	796	2	T32425	hypothetical prote
15	68	11.0	1474	2	B85188	retrotransposon li
16	68	11.0	2088	2	E71436	hypothetical prote
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18	67	10.8	187	2	T51876	hypothetical prote
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20	67	10.8	363	2	C86106	sensor protein for
21	67	10.8	363	2	JX0285	sensor protein bas
22	67	10.8	449	2	C39926	hypothetical 51.8K
23	67	10.8	519	2	G84707	probable MYB famil
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26	66.5	10.7	749	2	A75560	conserved hypothet
27	66	10.6	428	2	JH0634	site-specific DNA-
28	66	10.6	1001	2	T28897	hypothetical prote
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30	65.5	10.6	307	2	T33503	hypothetical prote
31	65	10.5	1027	2	B64187	conserved hypothet
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33	64.5	10.4	415	2	S32932	regulatory protein
34	64.5	10.4	708	2	A38436	mitosis initiation
35	64	10.3	188	2	T19507	hypothetical prote
36	64	10.3	354	2	G75548	ABC transporter, A
37	64	10.3	467	1	S45493	serine proteinase
38	64	10.3	502	2	T36589	probable transmemb
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40	64	10.3	637	2	T03842	fission yeast Skb1
41	64	10.3	695	2	T13648	mitosis initiation
42	64	10.3	749	2	S77175	sensory transducti
43	64	10.3	6805	2	S20901	titin - rabbit (fr
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ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: A59316
A;Status: not compared with conceptual translation
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A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
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F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 31.9%; Score 198; DB 1; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.8e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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ghrelin precursor - rat
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C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: B59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: B59316
A;Status: not compared with conceptual translation
A;Molecule type: mRNA; protein
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A;Cross-references: UNIPROT:Q9QYH7; GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g669
A;Experimental source: strain SD; tissue stomach endocrine cells

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A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

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  Matches   42;  Conservative    7;  Mismatches   34;  Indels   22;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              | |  |:|||||| |||:|:|||||||||||||: | |   | |      |   |   ||
Db          1 MVSSATICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP------PAKLQPRALE 54

Qy         61 QQRH-----:----------LWASVFSQSTKDSGSDLTVSGRTWG 89
                 |              : : |    | ||:     ||  |
Db         55 GWLHPEDRGQAEEAEEELEIRFNAPFDVGIKLSGAQYQQHGRALG 99


RESULT 3
AG0449
regulator of nucleoside diphosphate kinase rnk [imported] - Yersinia pestis (strain CO92
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0449
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0449
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: UNIPROT:Q8ZAU1; GB:AL590842; PIDN:CAC93163.1; PID:g15981613; GSPDB:G
C;Genetics:
A;Gene: rnk

  Query Match             12.6%;  Score 78;  DB 2;  Length 136;
  Best Local Similarity   26.2%;  Pred. No. 0.65;
  Matches   28;  Conservative   14;  Mismatches   39;  Indels   26;  Gaps    3;

Qy         21 AMAGS---SFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDL-EQQRHLWASVFSQSTKD 76
              | |||    : |: |  | :: ||:: |  |  :     :  ||   |: |:   |: | ||
Db         24 AFAGSVVATALNEELDRAEILPPNEIPADVVTMNSRVRFLDLNSQEEHIRTLVYPASLKD 83

Qy         77 SGSDLTV----------------------SGRTWGLRVLNRLFPPSS 101
                 |    |:|                      |    : ||  |: | |
Db         84 SNEQLSVMAPLGAALLGLHVNDEISWKLPGGDETRITVLELLYQPES 130


RESULT 4
T34274
hypothetical protein F46H5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34274
R;Nhan, M.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F46H5.
A;Reference number: Z21498
A;Accession: T34274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2018 <NHA>
A;Cross-references: UNIPROT:Q20487; EMBL:U41543; PIDN:AAB37023.1; GSPDB:GN00028; CESP:F4
A;Experimental source: strain Bristol N2; clone F46H5
C;Genetics:
A;Gene: CESP:F46H5.4

A;Map position: X
A;Introns: 16/2; 52/3; 87/2; 116/2; 138/2; 203/1; 265/3; 317/2; 337/3; 378/1; 428/1; 482/
7/3; 1491/3; 1560/2; 1632/2; 1753/3; 1830/2; 1862/2; 1927/3

  Query Match             11.9%;  Score 73.5;  DB 2;  Length 2018;
  Best Local Similarity   31.2%;  Pred. No. 38;
  Matches   25;  Conservative    7;  Mismatches   31;  Indels   17;  Gaps    4;

Qy         38 RPPHKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVS--GRTWGLRVLNR 95
              | ||    :  :||     |||    ||  :|:  | |:  |  | |  | ||
Db        652 RTPHFTDEIKLSLP-----CDLNDGHHLLFTVYHISCKEGDSSSTESPIGYTW------- 699

Qy         96 LFP--PSSRERSRRSHQPSC 113
                |   : : ||   | | |
Db        700 -LPLYRNGKLRSGNFHLPVC 718


RESULT 5
JC4335
anti-mullerian hormone type II receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 16-Aug-2004
C;Accession: JC4335
R;Visser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegoed,
Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995
A;Title: Structure and chromosomal localization of the human anti-muellerian hormone type
A;Reference number: JC4335; MUID:96028015; PMID:7488027
A;Accession: JC4335
A;Molecule type: mRNA
A;Residues: 1-573 <VIS>
A;Cross-references: UNIPROT:Q16671; GB:X91156; NID:g1107671; PIDN:CAA62593.1; PID:e198046
C;Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a crit
C;Genetics:
A;Gene: GDB:AMHR2
A;Cross-references: GDB:696210; OMIM:600956
A;Map position: 12q13-12q13
A;Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C;Superfamily: protein kinase homology
C;Keywords: ATP; hormone receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-573/Product: anti-muellerian hormone type II receptor #status predicted <MAT>
F;17-141/Domain: extracellular hormone binding #status predicted <ELB>
F;142-167/Domain: transmembrane #status predicted <TMM>
F;201-512/Domain: protein kinase homology <KIN>

  Query Match             11.8%;  Score 73;  DB 2;  Length 573;
  Best Local Similarity   27.4%;  Pred. No. 11;
  Matches   34;  Conservative   15;  Mismatches   35;  Indels   40;  Gaps    6;

Qy          3 SPGTVCS--------------LLLLGMLWLDLAMAGS---SFLSPEHQRVQVRP-PHKAP 44
              |||| |               |:|||:  | | : ||   : |  :: ||:  | |   |
Db        128 SPGTPGSQGPQAAPGESIWMALVLLGLFLLLLLVLGSIILALLQRKNYRVRGEPVPEPRP 187

Qy         45 H-------VVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLF 97
                     :  ||   :||           |||  :: |  :  :|:  |  |  : |
Db        188 DSGRDWSVELQELP---ELC------------FSQVIREGGHAVVWAGQLQGKLVAIKAF 232

Qy         98 PPSS 101
              || |
Db        233 PPRS 236


RESULT 6
E64211
virulence-associated protein vacB homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: E64211
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.M
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
```

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A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64211
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-725 <TIGR>
A;Cross-references: UNIPROT:P47350; GB:U39690; GB:L43967; NID:g1045782; PID:g1045783; TI
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: virulence-associated protein vacB homolog

  Query Match          11.8%;  Score 73;  DB 1;  Length 725;
  Best Local Similarity   25.7%;  Pred. No. 14;
  Matches   26;  Conservative   16;  Mismatches   39;  Indels   20;  Gaps    3;

Qy         18 LDLAMAGSSFLSPEHQRVQVRPPHKAP-------HVVPALP--LSNQLCDLEQQRHLWAS 68
                | :|:|  :     :  : :   ||         :||| ||  |||||| |   :  :
Db        298 LYVAIADVAHYVNRNSEIDIEAKHKTSSIYLPGHYVVPMLPEQLSNQLCSLNPAQKRYVV 357

Qy         69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSH 109
              |   |  : |  |           |:|:| :   ::| |:
Db        358 VCEISFDNQGRIKT----------NKLYPATIISKNRFSY 387


RESULT 7
H83043
hypothetical protein PA4822 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83043
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-555 <STO>
A;Cross-references: UNIPROT:Q9HUY8; GB:AE004895; GB:AE004091; NID:g9951083; PIDN:AAG0820
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4822

  Query Match          11.7%;  Score 72.5;  DB 2;  Length 555;
  Best Local Similarity   31.3%;  Pred. No. 12;
  Matches   31;  Conservative    9;  Mismatches   34;  Indels   25;  Gaps    4;

Qy          9 SLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQRHLWAS 68
              ||| | | |   : ||| |   |  |:             |||      :|:  ||  |
Db        420 SLLPLAMRWAGRSRAGSEF---ELGRM-------------LPLQ---AVIEESLHLAIS 459

Qy         69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRR 107
              | :   |:   |          ::| ||   :|||| ||
Db        460 AFLREDLDAALRLVAR-----KKLLQRLEADASRERFRR 493


RESULT 8
T22943
hypothetical protein F58G11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22943
R;Percy, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19640
A;Accession: T22943
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-666 <WIL>
A;Cross-references: UNIPROT:P90898; EMBL:Z81094; PIDN:CAB03154.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F58G11
C;Genetics:
A;Gene: CESP:F58G11.3
A;Map position: 5
A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3

  Query Match          11.6%;  Score 72;  DB 2;  Length 666;
  Best Local Similarity   26.9%;  Pred. No. 16;
  Matches   32;  Conservative   11;  Mismatches   42;  Indels   34;  Gaps    5;

Qy         33 QRVQVRPPHKAPHVVPALPLSNQLCDLEQQR-HLWASVFSQSTKDSGSD---------- 80
              |||:| |       |||   |   | :: :||  :    |::  : | |
Db        537 QRVRVNPNQCVKKVVPVRTLGQALAEVRRQREQVEQEAFNEQPEPSPSPRLGMGSSSHAA 596

Qy         81 LTVSGRTWGLRVLNR----------LFPPSS-------RERSR----RSHQPSCSPEL 117
                ||   || :|: :           | || |       | |||     |   |  | |
Db        597 SNVSDDGWGAQVVQKVEKSPPKPFTVLLPPMSKGAGVKIRPRSRVVLCHSSASSFPPSL 655


RESULT 9
I48882
thyrotropin receptor precursor - mouse
N;Alternate names: thyroid-stimulating hormone receptor; TSH receptor
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C;Accession: I48882
R;Stein, S.A.; Oates, E.L.; Hall, C.R.; Grumbles, R.M.; Fernandez, L.M.; Taylor, N.A.; P
Mol. Endocrinol. 8, 129-138, 1994
A;Title: Identification of a point mutation in the thyrotropin receptor of the hyt/hyt h
A;Reference number: A54271; MUID:94224232; PMID:8170469
A;Accession: I48882
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-764 <RES>
A;Cross-references: UNIPROT:P47750; EMBL:U02602; NID:g575923; PIDN:AAB60455.1; PID:g5759
C;Genetics:
A;Gene: TSHr
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h
C;Keywords: G protein-coupled receptor; transmembrane protein
F;53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

  Query Match          11.5%;  Score 71.5;  DB 2;  Length 764;
  Best Local Similarity   28.8%;  Pred. No. 21;
  Matches   32;  Conservative   16;  Mismatches   50;  Indels   13;  Gaps    4;

Qy          4 PGTVCSLLLLGMLWLDLAMAGSSFLSPE---HQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              ||::  |||: :| |  :: |     ||    ||     |   |  | :|:|| | |   |
Db          3 PGSL--LLLVLLLALSRSLRGKECASPPCECHQEDDFRVTCKELHRIPSLPPSTQTLKLI 60

Qy         61 QQ--RHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSH 109
              :   : : :  ||      |   |::          | || | |     |: :|
Db         61 ETHLKTIPSLAFSSLPNISRIYLSIDA------TLQRLEPHSFYNLSKMTH 105


RESULT 10
S77905
lyase - Pseudomonas pseudomallei
C;Species: Pseudomonas pseudomallei
C;Date: 21-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: S77905; S36445; S36446
R;Penaloza-Vazquez, A.; Mena, G.L.; Herrera-Estrella, L.; Bailey, A.M.
Appl. Environ. Microbiol. 61, 538-543, 1995
A;Title: Cloning and sequencing of the genes involved in glyphosphate utilization by Pse
A;Reference number: S77905; MUID:96031567; PMID:7574593
A;Accession: S77905
A;Molecule type: DNA
A;Residues: 1-309 <PEN>
A;Cross-references: UNIPROT:Q52502; EMBL:X74325; NID:g439726; PIDN:CAA52373.1; PID:g4397
```

```
A;Experimental source: strain 22
C;Genetics:
A;Gene: glpB
C;Superfamily: Pseudomonas pseudomallei lyase

  Query Match             11.4%;  Score 70.5;  DB 2;  Length 309;
  Best Local Similarity   22.0%;  Pred. No. 9.8;
  Matches   29;  Conservative   16;  Mismatches   36;  Indels   51;  Gaps    5;

Qy          2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPH--------VVPALPLS 53
              | || |                      ||  |:  : ||| || :        :| | | :
Db         14 PEPGIV-------------------LSGVHKSRRGRPPQKAAYLARWKYSPIVAADPRA 53

Qy         54 NQLCDLEQQRHLWASVFSQSTKDSGSDLT-----------VSGRTWGL----RVLNRLFP 98
               |         | | :    : :: ||  |             ::| :    |:||  |
Db         54 PQ--------HSWGNSRVDADRERGSTKTRNPNSREEVVICMSKSWNVNHEPRILNSQFA 105

Qy         99 PSSRERSRRSHQ 110
                |   :: ||:
Db        106 RKSLNAAKPSHR 117


RESULT 11
A56084
interleukin-1beta converting enzyme beta isozyme - human
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56084
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A;Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
A;Reference number: A56084; MUID:95181414; PMID:7876192
A;Accession: A56084
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-383 <ALN>
A;Cross-references: UNIPROT:P29466; GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
C;Genetics:
A;Gene: IL1BCE
C;Keywords: alternative splicing

  Query Match             11.4%;  Score 70.5;  DB 2;  Length 383;
  Best Local Similarity   22.0%;  Pred. No. 12;
  Matches   27;  Conservative   20;  Mismatches   37;  Indels   39;  Gaps    4;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSN------ 54
              :|      | : :  :    |  :||:  ||   | ||           ||:| |:
Db         62 IPKGAQACQICITYICEEDSYLAGTLGLSAAPQAVQDN---------PAMPTSSGSEGNV 112

Qy         55 QLCDLEQQRHLW----ASVFSQSTKDS--------------------GSDLTVSGRTWGL 90
              :|| ||: : :|    | ::    | |                    |::: ::| |  |
Db        113 KLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLL 172

Qy         91 RVL 93
              : |
Db        173 QNL 175


RESULT 12
H96792
unknown protein F14G6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96792
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96792
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <STO>
A;Cross-references: UNIPROT:Q9C9K7; GB:AE005173; NID:g6642668; PIDN:AAF20248.1; GSPDB:GN
C;Genetics:
A;Gene: F14G6.10
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200

  Query Match             11.1%;  Score 69;  DB 2;  Length 302;
  Best Local Similarity   31.6%;  Pred. No. 14;
  Matches   30;  Conservative    6;  Mismatches   31;  Indels   28;  Gaps    6;

Qy         30 PE-HQRVQVRPP-HKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRT 87
              || | ::| :|  |  |   |      |  | |           | | || |||   || |
Db         21 PELHHQLQPQPQLHPLPQPQPQPQPQQQNSDDE----------SDSNKDPGSDPVTSGST 70

Qy         88 WGLRVLNRLFPPSSRERSR------------RSH 109
              | |   |  || |: : :            |||
Db         71 -GKRPRGR--PPGSKNKPKPPVIVTRDSPNVLRSH 102


RESULT 13
S62048
probable membrane protein YGL197w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G1307
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S62048; S64214
R;Klima, R.; Coglievina, M.; Bertani, I.; Zaccaria, P.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A;Reference number: S62045
A;Accession: S62048
A;Molecule type: DNA
A;Residues: 1-1487 <KLI>
A;Cross-references: UNIPROT:P53094; EMBL:X91837; NID:g1177627; PID:e203620; PID:g1177631
A;Experimental source: strain FY1679
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64183
A;Accession: S64214
A;Molecule type: DNA
A;Residues: 1-1487 <BRU>
A;Cross-references: EMBL:Z72719; NID:g1322824; PID:e243500; PID:g1322825; MIPS:YGL197w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MDS3
A;Cross-references: SGD:S0003165; MIPS:YGL197w
A;Map position: 7L
C;Keywords: transmembrane protein
F;1034-1050/Domain: transmembrane #status predicted <TM1>
F;1052-1068/Domain: transmembrane #status predicted <TM2>

  Query Match             11.1%;  Score 69;  DB 2;  Length 1487;
  Best Local Similarity   25.7%;  Pred. No. 79;
  Matches   37;  Conservative   10;  Mismatches   37;  Indels   60;  Gaps    6;

Qy         25 SSFLSPEHQRVQVRPPHKAPHVVPALPL--------SNQLCDLEQ------QRHLWASVF 70
              ||    ||||        :| | : : ||          ||  |:|        ||    |
Db        769 SSISEAEHQR-------RASHPLTSSPLFEDSGTPCGKQLQQLQQHTIQNPHNHLSPRRF 821

Qy         71 SQSTKDSGSDLTVSGRTWG-----------------LRVLNRLFPPSSRE---------- 103
              |:| : | | :: |     |                 | |||   || :||
Db        822 SRSARSSISYVSSSSDRRGNSISSRSTSDSFGTPPVLGVLNVPLPPQTREPNEPPPPCPA 881

Qy        104 -----RSRRS-------HQPSCSP 115
                   :|||        |    ||
Db        882 MSTGSNTRRSNTLTDYMHSNKASP 905
```

```
RESULT 14
T32425
hypothetical protein C10E2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32425
R;Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C10E2.
A;Reference number: Z21165
A;Accession: T32425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-796 <WOH>
A;Cross-references: UNIPROT:O17323; EMBL:AF026202; PIDN:AAB71243.1; GSPDB:GN00028; CESP:
A;Experimental source: strain Bristol N2; clone C10E2
C;Genetics:
A;Gene: CESP:C10E2.3
A;Map position: X
A;Introns: 85/2; 220/2; 269/1; 305/1; 519/3; 576/3; 724/3; 755/3

  Query Match             11.0%;  Score 68;  DB 2;  Length 796;
  Best Local Similarity   28.6%;  Pred. No. 51;
  Matches   28;  Conservative   15;  Mismatches   35;  Indels   20;  Gaps    4;

Qy         18 LDLAMAGSSFLSPEHQRVQV-RPPHKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKD 76
              | || : :: ||  :  : | : | |  |  |  | ||: ||| :     ::  || |||
Db         47 LSLANSLTNLLSSSNGNLSVPQTPTKEHH--PTAPTSNRKCDLPRSN---STTISQLTKD 101

Qy         77 SGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCS 114
                        |: | :   |  | : :|:  | |
Db        102 --------------RLKNMIANRSKGESNSQSNLMSNS 125


RESULT 15
B85188
retrotransposon like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85188
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85188
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1474 <STO>
A;Cross-references: UNIPROT:O23529; GB:NC_001268; NID:g5302802; PIDN:CAB46043.1; GSPDB:G
C;Genetics:
A;Gene: dl4465c
A;Map position: 4
C;Superfamily: retrovirus-related polyprotein

  Query Match             11.0%;  Score 68;  DB 2;  Length 1474;
  Best Local Similarity   27.0%;  Pred. No. 1e+02;
  Matches   30;  Conservative   19;  Mismatches   42;  Indels   20;  Gaps    5;

Qy         16 LWLDLAMAGSSFL--SPEHQRVQVRPPHKAPHVV---PALPLSNQLCDLEQQRHLWASVF 70
              ::|  ::  :::|    ||:|:     : : |||    : | ||    |  |  |    |
Db        716 VFLGYSLTQTAYLCFDVEHKRL-----YTSRHVVFDEASFPFSN----LTSQNSLPTVTF 766

Qy         71 SQSTKD------SGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSP 115
               ||:        | | :  |  :    ||::  || :   |  | ||: ||
Db        767 EQSSSPLVTPILSSSSVLPSCLSSPCTVLHQQQPPVTTPNSPHSSQPTTSP 817


Search completed: July 26, 2005, 14:30:05
Job time : 42 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 26, 2005, 14:10:22 ; Search time 179 Seconds
(without alignments)
334.711 Million cell updates/sec

Title: US-10-659-782B-32
Perfect score: 620
Sequence: 1 MPSPGTVCSLLLLGMLWLDL.....PPSSRERSRRSHQPSCSPEL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	198	31.9	91	2	Q86YP8	Q86yp8 homo sapien
2	198	31.9	117	1	GHRL_HUMAN	Q9ubu3 homo sapien
3	194	31.3	117	2	Q6UDE7	Q6ude7 macaca mula
4	180	29.0	117	1	GHRL_FELCA	Q6beg6 felis silve
5	171.5	27.7	116	1	GHRL_CAPHI	Q6beg7 capra hircu
6	165	26.6	117	2	Q8CH53	Q8ch53 meriones un
7	163	26.3	117	1	GHRL_MOUSE	Q9eqx0 mus musculu
8	162	26.1	86	2	Q811T4	Q811t4 mus musculu
9	162	26.1	117	1	GHRL_CANFA	Q9bef8 canis famil
10	158.5	25.6	78	2	Q7TSD1	Q7tsd1 mus musculu
11	158	25.5	117	1	GHRL_RAT	Q9qyh7 rattus norv
12	157.5	25.4	116	2	Q863L0	Q8631o ovis aries
13	150.5	24.3	74	2	Q67BB5	Q67bb5 sus scrofa
14	150.5	24.3	118	1	GHRL_PIG	Q9gky5 sus scrofa
15	147	23.7	54	2	Q6SLG1	Q6slg1 capra hircu
16	146	23.5	54	2	Q6SLF6	Q6slf6 cervus elap
17	145.5	23.5	116	1	GHRL_BOVIN	Q9bdj6 bos taurus
18	145	23.4	52	2	Q6SLF9	Q6slf9 odocoileus
19	145	23.4	54	2	Q6SLF2	Q6slf2 odocoileus
20	145	23.4	54	2	Q6SLF8	Q6slf8 rangifer ta
21	142	22.9	54	2	Q6SLF4	Q6slf4 alces alces
22	135.5	21.9	65	2	Q6TGF0	Q6tgf0 sus scrofa
23	133	21.5	54	2	Q6SLG3	Q6slg3 ovis aries
24	130	21.0	54	2	Q6SPC2	Q6spc2 bison bison
25	122.5	19.8	54	2	Q6SLG5	Q6slg5 kogia brevi
26	122.5	19.8	54	2	Q6SLG7	Q6slg7 bos taurus
27	113.5	18.3	97	2	Q863C6	Q863c6 ovis aries
28	101	16.3	35	2	Q6SPC3	Q6spc3 antilocapra
29	98.5	15.9	116	2	Q6VMJ7	Q6vmj7 anser sp. (
30	95	15.3	114	2	Q6F4B4	Q6f4b4 trachemys s
31	95	15.3	124	2	Q6F4B3	Q6f4b3 trachemys s
32	93	15.0	116	2	Q6VMJ5	Q6vmj5 dromaius no
33	93	15.0	116	2	Q6VMJ6	Q6vmj6 anas platyr
34	81	13.1	100	2	O52856	O52856 bacillus su
35	78	12.6	136	2	Q665H9	Q665h9 yersinia ps
36	78	12.6	136	2	Q8ZAU1	Q8zau1 yersinia pe
37	78	12.6	1218	2	Q9W201	Q9w201 drosophila
38	76	12.3	1222	1	WNK4_MOUSE	Q80ue6 mus musculu
39	75.5	12.2	208	2	Q6V501	Q6v501 oryctolagus
40	75	12.1	116	2	Q7T2V1	Q7t2v1 gallus gall
41	75	12.1	116	2	Q8AV73	Q8av73 gallus gall
42	74	11.9	256	2	Q8S2J0	Q8s2j0 oryza sativ
43	74	11.9	478	2	Q647K2	Q647k2 homo sapien
44	74	11.9	573	1	AMH2_HUMAN	Q16671 homo sapien
45	74	11.9	1688	2	Q7QBB6	Q7qbb6 anopheles g

ALIGNMENTS

RESULT 1
Q86YP8
ID Q86YP8 PRELIMINARY; PRT; 91 AA.
AC Q86YP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exon 3-deleted preproghrelin variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeffery P.L., Herington A.C., Chopin L.K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY184207; AAO27351.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.
DR InterPro; IPR011070; AlphaBeta_subunt.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
SQ SEQUENCE 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;

Query Match 31.9%; Score 198; DB 2; Length 91;
Best Local Similarity 88.6%; Pred. No. 1.4e-12;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
```

RESULT 2
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3; Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein)
DE (UNQ524/PRO1066).
GN Name=GHRL; Synonyms=MTLRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;

```
RA   Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT   "Ghrelin is a growth-hormone-releasing acylated peptide from
RT   stomach.";
RL   Nature 402:656-660(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA   Kojima M.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Stomach;
RA   Tomasetto C., Karam S.M., Rio M.-C.;
RT   "Identification of a novel gastric protein m46.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L.;
RT   "Genomic organization of the human Ghrelin gene.";
RL   J. Endocr. Genet. 1:231-233(2000).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Blood;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 24-33.
RC   TISSUE=Stomach;
RX   MEDLINE=20389976; PubMed=10930375;
RA   Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA   Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT   "Identification and characterization of a novel gastric peptide
RT   hormone: the motilin-related peptide.";
RL   Gastroenterology 119:395-405(2000).
RN   [8]
RP   SEQUENCE OF 24-38.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [9]
RP   REVIEW.
RX   MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA   Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT   "Ghrelin: discovery of the natural endogenous ligand for the growth
RT   hormone secretagogue receptor.";
RL   Trends Endocrinol. Metab. 12:118-122(2001).
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q9UBU3-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q9UBU3-2; Sequence=VSP_003245;
CC   -!- PTM: O-n-octanoylation is essential for activity.
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/GhrelinID327.html".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB029434; BAA89371.1; -.
DR   EMBL; AB035700; BAB19045.1; -.
DR   EMBL; AJ252278; CAB65733.1; -.
DR   EMBL; AF296558; AAG10300.1; -.
DR   EMBL; AY359053; AAQ89412.1; -.
DR   EMBL; BC025791; AAH25791.1; -.
DR   PIR; A59316; A59316.
DR   H-InvDB; HIX0003050; -.
DR   MIM; 605353; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005131; F:growth hormone receptor binding; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT   SIGNAL        1     23
FT   PEPTIDE      24     51       Ghrelin.
FT   PROPEP       52    117       Removed in mature form.
FT   LIPID        26     26       O-octanoyl serine.
FT   VARSPLIC     37     37       Missing (in isoform 2).
FT                                /FTId=VSP_003245.
FT   CONFLICT     72     72       L -> M (in Ref. 6).
SQ   SEQUENCE   117 AA;  12911 MW;  39C0572EBECA2755 CRC64;

  Query Match             31.9%;  Score 198;  DB 1;  Length 117;
  Best Local Similarity   88.6%;  Pred. No. 1.9e-12;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||||||| |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
```

```
RESULT 3
Q6UDE7
ID   Q6UDE7      PRELIMINARY;      PRT;   117 AA.
AC   Q6UDE7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ghrelin.
GN   Name=GHRL;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14736731; DOI=10.1210/en.2003-1103;
RA   Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA   Suomi S., Hansen B.C.;
RT   "Characterization of the rhesus monkey ghrelin gene and factors
RT   influencing ghrelin gene expression and fasting plasma levels.";
RL   Endocrinology 145:2197-2205(2004).
DR   EMBL; AY372274; AAQ74837.1; -.
DR   EMBL; AY371699; AAQ74381.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   GO; GO:0050791; P:regulation of physiological process; IEA.
DR   InterPro; IPR011070; AlphaBeta_subunt.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
SQ   SEQUENCE   117 AA;  12913 MW;  1B634ACE1E1F19FF CRC64;

  Query Match             31.3%;  Score 194;  DB 2;  Length 117;
  Best Local Similarity   86.4%;  Pred. No. 4.9e-12;
  Matches   38;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||||||||||||||||||||||| | |   | |
Db          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRAQQRKESKKP 44


RESULT 4
GHRL_FELCA
ID   GHRL_FELCA     STANDARD;      PRT;   117 AA.
AC   Q6BEG6; Q6BEG5;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide).
GN   Name=GHRL;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RA   Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
RT   "cDNA cloning of feline and caprine ghrelin.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q6BEG6-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q6BEG6-2; Sequence=VSP_011626;
CC   -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; AB089201; BAD34670.1; -.
DR   EMBL; AB089202; BAD34671.1; -.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues; Hormone;
KW   Lipoprotein; Signal.
FT   SIGNAL        1     23       By similarity.
FT   PEPTIDE      24     51       Ghrelin (By similarity).
FT   PROPEP       52    117       Removed in mature form (By similarity).
FT   LIPID        26     26       O-octanoyl serine (By similarity).
FT   VARSPLIC     37     37       Missing (in isoform 2).
FT                                /FTId=VSP_011626.
SQ   SEQUENCE   117 AA;  12956 MW;  8235A51447FFF530 CRC64;

  Query Match             29.0%;  Score 180;  DB 1;  Length 117;
  Best Local Similarity   79.5%;  Pred. No. 1.3e-10;
  Matches   35;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              |||||||||||  ||| ||||||||||||||:|| |   | |
Db          1 MPSPGTVCSLLLFSMLWADLAMAGSSFLSPEHQKVQQRKESKKP 44


RESULT 5
GHRL_CAPHI
ID   GHRL_CAPHI     STANDARD;      PRT;   116 AA.
AC   Q6BEG7;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide).
GN   Name=GHRL;
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RA   Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
RT   "cDNA cloning of feline and caprine ghrelin.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB089200; BAD34669.1; -.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Cleavage on pair of basic residues; Hormone; Lipoprotein; Signal.
FT   SIGNAL        1     23       By similarity.
FT   PEPTIDE      24     50       Ghrelin (By similarity).
FT   PROPEP       51    116       Removed in mature form (By similarity).
FT   LIPID        26     26       O-octanoyl serine (By similarity).
SQ   SEQUENCE   116 AA;  12935 MW;  CDA67971D72E3303 CRC64;

  Query Match             27.7%;  Score 171.5;  DB 1;  Length 116;
  Best Local Similarity   42.9%;  Pred. No. 9.7e-10;
  Matches   42;  Conservative   13;  Mismatches   34;  Indels    9;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL 59
              ||:| |:|||||| |||:||||||||||||||::| : | |    :    | |   |:
Db          1 MPAPRTICSLLLLSMLWMDLAMAGSSFLSPEHQKLQRKEPKKPSGRLKPRALEGQFDPDV 60

Qy         60 EQQRH--------LWASVFSQSTKDSGSDLTVSGRTWG 89
                |           : : |:   | ||:     |:| |
Db         61 GSQEEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLG 98


RESULT 6
Q8CH53
ID   Q8CH53      PRELIMINARY;      PRT;   117 AA.
AC   Q8CH53;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ghrelin preproprotein.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14724148; DOI=10.1136/gut.2003.021568;
RA   Suzuki H., Masaoka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
RA   Kangawa K., Ishii H.;
RT   "Helicobacter pylori infection modifies gastric and plasma ghrelin
RT   dynamics in Mongolian gerbils.";
RL   Gut 53:187-194(2004).
DR   EMBL; AF442491; AAO06965.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   GO; GO:0050791; P:regulation of physiological process; IEA.
DR   InterPro; IPR011070; AlphaBeta_subunt.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
SQ   SEQUENCE   117 AA;  13035 MW;  27657687FC026A74 CRC64;

  Query Match             26.6%;  Score 165;  DB 2;  Length 117;
  Best Local Similarity   41.0%;  Pred. No. 4.6e-09;
  Matches   43;  Conservative    8;  Mismatches   32;  Indels   22;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              | | ||:|||||||:||:|:|||||||||||||: | |   | |       |   |   ||
Db          1 MMSSGTICSLLLLGVLWMDVAMAGSSFLSPEHQKTQQRKESKKP------PAKLQPRALE 54

Qy         61 QQRH----------------LWASVFSQSTKDSGSDLTVSGRTWG 89
                |                  : : |    | ||:     ||  |
Db         55 GWLHPDGRGQAEGAEDELEIRFNAPFDVGIKLSGAQYQQHGRALG 99
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RESULT 7
GHRL_MOUSE
ID   GHRL_MOUSE     STANDARD;      PRT;   117 AA.
AC   Q9EQX0; Q9WUZ1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide) (M46 protein).
GN   Name=Ghrl; Synonyms=Mtlrp;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC   TISSUE=Stomach;
RX   MEDLINE=20389976; PubMed=10930375;
RA   Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA   Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT   "Identification and characterization of a novel gastric peptide
RT   hormone: the motilin-related peptide.";
RL   Gastroenterology 119:395-405(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Kojima M.;
RT   "Mouse mRNA for preproghrelin.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6J; TISSUE=Stomach;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   REVIEW.
RX   MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA   Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT   "Ghrelin: discovery of the natural endogenous ligand for the growth
RT   hormone secretagogue receptor.";
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RL   Trends Endocrinol. Metab. 12:118-122(2001).
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q9EQX0-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC   -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC       with higher levels in the stomach, medium levels in the duodenum,
CC       jejunum, ileum and colon. Low expression in the testis and brain.
CC       Not detected in the salivary gland, pancreas, liver and lung.
CC   -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ243503; CAB46500.1; -.
DR   EMBL; AB035701; BAB19046.1; -.
DR   EMBL; AB060078; BAB69857.1; -.
DR   EMBL; AK008658; BAB25814.1; -.
DR   EMBL; AK008860; BAB25934.1; -.
DR   MGD; MGI:1930008; Ghrl.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT   SIGNAL        1     23
FT   PEPTIDE      24     51       Ghrelin.
FT   PROPEP       52    117       Removed in mature form (By similarity).
FT   LIPID        26     26       O-octanoyl serine (By similarity).
FT   VARSPLIC     37     37       Missing (in isoform 2).
FT                                /FTId=VSP_003246.
SQ   SEQUENCE   117 AA;  13207 MW;  EACB49D2E3CA7203 CRC64;

  Query Match             26.3%;  Score 163;  DB 1;  Length 117;
  Best Local Similarity   41.0%;  Pred. No. 7.3e-09;
  Matches   43;  Conservative    7;  Mismatches   33;  Indels   22;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              | | ||:|||||| |||:|:||||||||||||||: | |   | |       |   |   ||
Db          1 MLSSGTICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP------PAKLQPRALE 54

Qy         61 QQRH----------------LWASVFSQSTKDSGSDLTVSGRTWG 89
                |                : : |    | ||:     ||  |
Db         55 GWLHPEDRGQAEETEEELEIRFNAPFDVGIKLSGAQYQQHGRALG 99


RESULT 8
Q811T4
ID   Q811T4      PRELIMINARY;      PRT;    86 AA.
AC   Q811T4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Exon 4-deleted preproghrelin variant.
GN   Name=Ghrl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Swiss;
RA   Jeffery P.L., Herington A.C., Chopin L.K.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY179430; AAO27350.1; -.
DR   MGD; MGI:1930008; Ghrl.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   InterPro; IPR011070; AlphaBeta_subunt.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
SQ   SEQUENCE   86 AA;  9758 MW;  B913858874770512 CRC64;

  Query Match             26.1%;  Score 162;  DB 2;  Length 86;
  Best Local Similarity   70.5%;  Pred. No. 6.5e-09;
  Matches   31;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              | | ||:|||||| |||:|:||||||||||||||: | |   | |
Db          1 MLSSGTICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP 44


RESULT 9
GHRL_CANFA
ID   GHRL_CANFA     STANDARD;      PRT;   117 AA.
AC   Q9BEF8; Q9BEF7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide).
GN   Name=GHRL; Synonyms=MTLRP;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Gastric fundus;
RA   Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
RT   "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT   fundus.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q9BEF8-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC   -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ298295; CAC29155.1; -.
DR   EMBL; AJ298296; CAC29156.1; -.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues; Hormone;
KW   Lipoprotein; Signal.
FT   SIGNAL        1     23       By similarity.
FT   PEPTIDE      24     51       Ghrelin (By similarity).
FT   PROPEP       52    117       Removed in mature form (By similarity).
FT   LIPID        26     26       O-octanoyl serine (By similarity).
FT   VARSPLIC     37     37       Missing (in isoform 2).
FT                                /FTId=VSP_003244.
SQ   SEQUENCE   117 AA;  13007 MW;  3E57FED9D1847CF7 CRC64;

  Query Match             26.1%;  Score 162;  DB 1;  Length 117;
  Best Local Similarity   70.5%;  Pred. No. 9.2e-09;
  Matches   31;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
              ||| ||:|||||  :||:||||||||||||||::| |   | |
Db          1 MPSLGTMCSLLLFSVLWVDLAMAGSSFLSPEHQKLQQRKESKKP 44


RESULT 10
Q7TSD1
ID   Q7TSD1      PRELIMINARY;      PRT;    78 AA.
AC   Q7TSD1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ghrelin delta2.
GN   Name=Ghrelin;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hisatomi H., Nagao K., Hirata H., Kawano K., Hibi N.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB111891; BAC77409.1; -.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   ProDom; PD332162; Preproghrelin; 1.
SQ   SEQUENCE   78 AA;  8615 MW;  AD87CB53C9A22FFB CRC64;

  Query Match             25.6%;  Score 158.5;  DB 2;  Length 78;
  Best Local Similarity   40.7%;  Pred. No. 1.3e-08;
  Matches   37;  Conservative   11;  Mismatches   18;  Indels   25;  Gaps    3;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              | | ||:|||||| |||:|:|||||||||||||: |   |          :  :|  :
Db          1 MLSSGTICSLLLLSMLWMDMAMAGSSFLSPEHQKAQFNAP---------FDVGIKLSGAQ 51

Qy         61 QQRH-----------LWASVFSQSTKDSGSD 80
               |:|           ||  |     |:: :|
Db         52 YQQHGRALGKFLQDILWEEV-----KEAPAD 77


RESULT 11
GHRL_RAT
ID   GHRL_RAT       STANDARD;      PRT;   117 AA.
AC   Q9QYH7; Q9ET69;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide).
GN   Name=Ghrl;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
RP   AND ACYLATION OF SER-26.
RC   STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX   MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA   Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT   "Ghrelin is a growth-hormone-releasing acylated peptide from
RT   stomach.";
RL   Nature 402:656-660(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
RP   SPECTROMETRY, AND ACYLATION OF SER-26.
RC   STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX   MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
RA   Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT   "Purification and characterization of rat des-Gln14-ghrelin, a second
RT   endogenous ligand for the growth hormone secretagogue receptor.";
RL   J. Biol. Chem. 275:21995-22000(2000).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
RA   Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT   "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT   in gastrointestinal tissue.";
RL   Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN   [4]
RP   STRUCTURE-ACTIVITY RELATIONSHIP.
RX   MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
RA   Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA   Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT   "Structure-activity relationship of ghrelin: pharmacological study of
RT   ghrelin peptides.";
RL   Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN   [5]
RP   REVIEW.
RX   MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA   Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT   "Ghrelin: discovery of the natural endogenous ligand for the growth
RT   hormone secretagogue receptor.";
RL   Trends Endocrinol. Metab. 12:118-122(2001).
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q9QYH7-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC   -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC       the stomach. Very low levels are detected in the hypothalamus,
CC       heart, lung, pancreas, intestine and adipose tissue.
CC   -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC       of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC   -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC       RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
CC   -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC       RANGE=24-50 (Q9QYH7-2); NOTE=Ref.2.
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CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB029433; BAA89370.1; -.
DR   EMBL; AB035699; BAB11956.1; -.
DR   PIR; B59316; B59316.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT   SIGNAL       1     23
FT   PEPTIDE      24    51       Ghrelin.
FT   PROPEP       52    117      Removed in mature form.
FT   LIPID        26    26       O-octanoyl serine.
FT   VARSPLIC     37    37       Missing (in isoform 2).
FT                               /FTId=VSP_003248.
SQ   SEQUENCE   117 AA;  13176 MW;  8857546FE51A7691 CRC64;

  Query Match             25.5%;  Score 158;  DB 1;  Length 117;
  Best Local Similarity   40.0%;  Pred. No. 2.4e-08;
  Matches   42;  Conservative    7;  Mismatches   34;  Indels   22;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE 60
              | |  |:|||||| |||:|:|||||||||||||: | |   | |      |   |   ||
Db          1 MVSSATICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP------PAKLQPRALE 54

Qy         61 QQRH---------------LWASVFSQSTKDSGSDLTVSGRTWG 89
                |                 : : |    | ||:     ||  |
Db         55 GWLHPEDRGQAEEAEEELEIRFNAPFDVGIKLSGAQYQQHGRALG 99


RESULT 12
Q863L0
ID   Q863L0      PRELIMINARY;      PRT;   116 AA.
AC   Q863L0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Preproghrelin precursor.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RA   Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB060699; BAC75928.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   GO; GO:0050791; P:regulation of physiological process; IEA.
DR   InterPro; IPR011070; AlphaBeta_subunt.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Signal.
FT   SIGNAL       1     23       Potential.
FT   CHAIN        24    50       ghrelin.
SQ   SEQUENCE   116 AA;  12977 MW;  B78ECA3DBF0E568E CRC64;

  Query Match             25.4%;  Score 157.5;  DB 2;  Length 116;
  Best Local Similarity   40.8%;  Pred. No. 2.6e-08;
  Matches   40;  Conservative   14;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL 59
              ||:| |: ||||| :||:|||||||||||||||::| : | |    :    | |   |:
Db          1 MPAPRTIYSLLLLSLLWMDLAMAGSSFLSPEHQKLQRKEPKKPSGRLKPRALEGQFDPDV 60

Qy         60 EQQRH--------LWASVFSQSTKDSGSDLTVSGRTWG 89
                |              : : |:   | ||:     |:| |
Db         61 GSQEEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLG 98


RESULT 13
Q67BB5
ID   Q67BB5      PRELIMINARY;      PRT;    74 AA.
AC   Q67BB5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Ghrelin (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kim K.-S., Rothschild M.F.;
RT   "Pig Ghrelin.";
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY373019; AAR24571.1; -.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
FT   NON_TER      74     74
SQ   SEQUENCE   74 AA;  7980 MW;  875424C2D41FC166 CRC64;

  Query Match             24.3%;  Score 150.5;  DB 2;  Length 74;
  Best Local Similarity   71.1%;  Pred. No. 8.3e-08;
  Matches   32;  Conservative    4;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 MPSPGTVCSLLLLGMLWL-DLAMAGSSFLSPEHQRVQVRPPHKAP 44
              ||| ||:|||||| :| : |||||||||||||||:|| |   | |
Db          1 MPSTGTICSLLLLSVLLMADLAMAGSSFLSPEHQKVQQRKESKKP 45


RESULT 14
GHRL_PIG
ID   GHRL_PIG       STANDARD;      PRT;   118 AA.
AC   Q9GKY5; Q9BDG8; Q9GKY4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE   releasing peptide) (Motilin-related peptide).
GN   Name=GHRL;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA   Kojima M.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Stomach;
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RA   Rousselle J., Lacroix D., Dubreuil P.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC       receptor type 1 (GHSR) inducing the release of growth hormone from
CC       the pituitary. Has an appetite-stimulating effect, induces
CC       adiposity and stimulates gastric acid secretion. Involved in
CC       growth regulation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Ghrelin;
CC         IsoId=Q9GKY5-1; Sequence=Displayed;
CC       Name=2; Synonyms=del-Gln14-ghrelin;
CC         IsoId=Q9GKY5-2; Sequence=VSP_003247;
CC   -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC   -!- SIMILARITY: Belongs to the motilin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB035703; BAB19048.1; -.
DR   EMBL; AB035704; BAB19049.1; -.
DR   EMBL; AF308930; AAK19243.1; -.
DR   EMBL; AY028942; AAK30002.1; -.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Alternative splicing; Cleavage on pair of basic residues; Hormone;
KW   Lipoprotein; Signal.
FT   SIGNAL       1     24       By similarity.
FT   PEPTIDE      25    52       Ghrelin.
FT   PROPEP       53    118      Removed in mature form (By similarity).
FT   LIPID        27    27       O-octanoyl serine (By similarity).
FT   VARSPLIC     38    38       Missing (in isoform 2).
FT                               /FTId=VSP_003247.
FT   CONFLICT     17    17       L -> P (in Ref. 2; AAK30002).
FT   CONFLICT     72    72       K -> E (in Ref. 2; AAK30002).
SQ   SEQUENCE   118 AA;  12785 MW;  856D3E1D6DAB1A76 CRC64;

  Query Match             24.3%;  Score 150.5;  DB 1;  Length 118;
  Best Local Similarity   71.1%;  Pred. No. 1.4e-07;
  Matches   32;  Conservative    4;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 MPSPGTVCSLLLLGMLWL-DLAMAGSSFLSPEHQRVQVRPPHKAP 44
              ||| ||:|||||| :| : |||||||||||||||:|| |   | |
Db          1 MPSTGTICSLLLLSVLLMADLAMAGSSFLSPEHQKVQQRKESKKP 45


RESULT 15
Q6SLG1
ID   Q6SLG1      PRELIMINARY;      PRT;    54 AA.
AC   Q6SLG1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ghrelin (Fragment).
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dickin J.C., Thue T.D., Buchanan F.C.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY455985; AAS67351.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   GO; GO:0050791; P:regulation of physiological process; IEA.
DR   InterPro; IPR006738; motilin_ghrelin.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04644; Motilin_ghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
FT   NON_TER      1     1
FT   NON_TER      54    54
SQ   SEQUENCE   54 AA;  6095 MW;  C77F81F0BE0B5E98 CRC64;

  Query Match             23.7%;  Score 147;  DB 2;  Length 54;
  Best Local Similarity   75.0%;  Pred. No. 1.3e-07;
  Matches   27;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 VCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHK 42
              :|||||| |||:|||||||||||||||::| : | |
Db          1 ICSLLLLSMLWMDLAMAGSSFLSPEHQKLQRKEPKK 36


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